

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 06:46:44 ; Search time 14302.9 Seconds
(without alignments)
1479.199 Million cell updates/sec

Title: US-09-294-298-3
Perfect score: 4134
Sequence: 1 taagggccccccccccgacc.....tggggtgctatccccatcct 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl:*
1: gb_bal:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
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10: gb_pr3:*
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- 44: gb_pl3:*
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74: gb_ro:*
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76: gb_sts2:*
77: gb_sy:*
78: gb_un:*
79: gb_vil:*
80: gb_vil2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	4118.8	99.6	4140	74	AF058790	AF058790 Rattus no
2	3919	94.8	4265	74	AF050183	AF050183 Rattus no
3	3907.4	94.5	4539	74	AF058789	AF058789 Rattus no
4	3680.4	89.0	4063	74	AF048976	AF048976 Rattus no
5	3602.8	87.2	4801	74	AB016962	AB016962 Rattus no
6	920.8	22.3	94770	69	HSDJ570F3	AL050332 Human DNA
7	920.8	22.3	150956	70	AL161903	AL161903 Homo sapi
8	920.8	22.3	169323	70	AL161906	AL161906 Homo sapi
9	629	15.2	829	74	AF053938	AF053938 Rattus no
10	627.8	15.2	4368	10	AF047711	AF047711 Homo sapi
11	336.4	8.1	4287	34	AK024488	AK024488 Homo sapi
12	241.8	5.8	56366	39	AC019800	AC019800 Drosophil
13	241.8	5.8	191504	36	AC012162	AC012162 Drosophil
14	241.8	5.8	202741	36	AC012161	AC012161 Drosophil
15	241.8	5.8	300994	28	AE003506	AE003506 Drosophil
16	236.8	5.7	3984	28	AB011280	AB011280 Caenorhab
17	223.6	5.4	65961	38	AC016523	AC016523 Drosophil
18	205.2	5.0	2385	34	AK022662	AK022662 Homo sapi
19	196	4.7	172027	72	AL365274	AL365274 Homo sapi
20	194.4	4.7	211	74	AF055883	AF055883 Rattus no
21	187.6	4.5	169323	70	AL161906	AL161906 Homo sapi

Chera

C	22	157	3.8	81971	68	HS593C16	AL035702	Human	DNA
	23	157	3.8	156700	50	AC027051	AC027051	Homo sapi	
	24	139.2	3.4	155332	51	AC040900	AC040900	Homo sapi	
c	25	139.2	3.4	156700	50	AC027051	AC027051	Homo sapi	
	26	113.4	2.7	4107	74	MMU20238	U20238	Mus musculu	
	27	103.4	2.5	159777	35	AC011703	AC011703	Drosophil	
	28	103.2	2.5	157803	35	AC011492	AC011492	Homo sapi	
	29	100	2.4	39660	29	CEC07B5	Z46266	Caenorhabdi	
	30	99.2	2.4	2837	69	HSINSP4BP	X89399	Homo sapien	
	31	98.4	2.4	237619	56	AC073765	AC073765	Mus muscu	
	32	97.6	2.4	833	28	AB011285	AB011285	Caenorhab	
	33	95.8	2.3	2647	81	E13125	E13125	Bovine gene	
	34	95.8	2.3	2730	3	BTU30857	U30857	Bos taurus	
	35	93.8	2.3	760	28	AB011283	AB011283	Caenorhab	
	36	93.8	2.3	2276	28	AB011279	AB011279	Caenorhab	
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	38	71.2	1.7	310	28	AB011284	AB011284	Caenorhab	
c	39	70.8	1.7	5719	74	MMCATS1	AF051726	Mus muscu	
c	40	70.8	1.7	180385	9	AC007461	AC007461	Homo sapi	
c	41	69.6	1.7	3720	80	S76368	S76368	ORF 5' of E	
c	42	69.6	1.7	43658	80	HSV3PRGEN	M86409	Herpesvirus	
c	43	69.6	1.7	112930	80	HSGEND	X64346	Herpesvirus	
	44	68	1.6	5579	8	AB011110	AB011110	Homo sapi	
c	45	67.4	1.6	314556	56	AC073495	AC073495	Mus muscu	

ALIGNMENTS

RESULT	1								
AF058790	AF058790	4140 bp	mRNA	ROD	09-OCT-1998				
LOCUS	Rattus norvegicus	SynGAP-b	complete cds.						
DEFINITION	Rattus norvegicus	SynGAP-b	complete cds.						
ACCESSION	AF058790								
VERSION	AF058790.1	GI:3722228							
KEYWORDS	Norway rat.								
SOURCE	Rattus norvegicus								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
REFERENCE	1 (bases 1 to 4140)								
AUTHORS	Kim,J.H., Liao,D., Lau,L.F. and Huganir,R.L.								
TITLE	SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family								
JOURNAL	Neuron 20 (4), 683-691 (1998)								
MEDLINE	98240917								
REFERENCE	2 (bases 1 to 4140)								
AUTHORS	Kim,J.H. and Huganir,R.L.								
TITLE	Direct Submission								
JOURNAL	Submitted (09-APR-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA								
REFERENCE	3 (bases 1 to 4140)								
AUTHORS	Kim,J.H. and Huganir,R.L.								
TITLE	Direct Submission								
JOURNAL	Submitted (08-OCT-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA								
REMARK	Sequence update by submitter								
COMMENT	On Oct 9, 1998 this sequence version replaced gi:3065890.								
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source	1. .4140								
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	/tissue_type="hippocampus"								
	1. .3750								
	/note="neuronal RasGAP; contains PH domain, C2 domain, GAP domain in the N-terminal region, and a T/SXV motif at the C-terminus"								
	/codon_start=1								
	/product="SynGAP-b"								
	/protein_id="AAC63511.1"								
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	/translation="MGLRPPTPTPSGGSGSLPPPSHRQPLRRRCSSCCFPGEYHLG								
CDS									

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	REFSADHRRARLMQSFKESHESLLSPSSAAEALELNLEDSIIKPVHSSILGOEFC			
	FEVTSSTGKCFACRSAERDKWIENLQRAVKPNKDNRRVDNVKLWII EARELPPK			
	KRYICELCLDDMLYARTTSKPRSASGDTVFWEHFEFNLPVRAIRLHLRYRDSDKKR			
	KKDKAGYVGLVTVPVATLAGRHTEQWYPTVLTPTSGSGGSGGGSGGGSGGGK			
	KGGCPAVRLKARYQTMILPMELYKEFAEYVTNHYMLCAVLEPALNVKKEEAVASAL			
	VHILQSTGKAKDFLSDMAMSEVDPRPKTASSLAEHQANLRMCCELALCKVNVSHCVFPRELKE			
	IGEFIRALYEESEENCEVDPIKCTASSLAEHQANLRMCCELALCKVNVSHCVFPRELKE			
	VFAWRRLRCAERGEDIAADRLISASLFLRFLCPAIMSQFLFGLMQLFDEQTPDEOTSRTLT			
	IAKVIQNLANFSKFTSKEDFLGFMNEFLELEWGSQQOFLYEISNLDLTLTNSSSFEYI			
	DIIGRELSTLHALLWEVLPQLSKEALLKGLPLRLLSLDSTALRNPNIQRPQRSQSER			
	RSQPMVLRGPSAEMQGYMMDLNSSIDLQSFMARGNLSSMDMARLPSPTEKPPPPPP			
	GGGKDLFYVSRPPLARSSPAYCTSSSDITEPEQKMLSVNKSVMLDLQGDGPGGRLNS			
	SSVSNLAAVGDLLHSSQASLTAAALGLRPAPAGRLSQSGSSSITAAGMRLSQMGVTTDG			
	VPAQQLRIPLPSFQNLFLHMAADGPGPPAGHGGSSGGHGGPPSSHHHHHHHRRGGEPPG			
	DTFAPFHGYKSEDLSTGVKPPPAASILHSHSYSDEFGSGTDFTRRQLSLQDNLOHM			
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	MPASERTVAWVSNMPHLSADIESAHIEREYKLYKESKSMDESRLDRVKEYEIEIHS			
	KERLHMSNRKLEEYERRLLSQEEQTSKILMQYQARLEQSEKRLRQQQVEKDSQIKSII			
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Query Match	99.6%;	Score 4118.8;	DB 74;	Length 4140;
Best Local Similarity	99.9%;	Pred. No. 0;		
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			Indels	1;
			Gaps	1;
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Qy	61	ccacccgcagcctctccgcgcgtgctcttccctgctgctgtcttccggttccttccttcctt	120	
Db	68	CCCACCGCAGCCTCTCCGCCCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	127	
Qy	121	tgggtcgctcgaggaggaggagagtggtccccggggttccttccttccttccttccttccttc	180	
Db	128	TGGGTCTGCTCGAGGAGGAGAGTGT-CCCCGGGGGGAAACAGTACAGCATGGAAGCCGCC	186	
Qy	181	ccgctgcgcccttcctcgcccttcgaaaggcttccttccttccttccttccttccttccttc	240	
Db	187	CCCCGTGCGCCCTTCCGGCCCTCGCAAGGCTTCTGAGCCCGGAGGCTAAAAAGCTCCATC	246	
Qy	241	aaacgtacaaaagtcacaaacccaaacttgaccggaccagcagcttccttccttccttccttc	300	
Db	247	AAACGTACAAAGTCACAAACCCAACTTGACCCGACACAGCAGCTTCGACAGATCCTGCCT	306	
Qy	301	cgcttcgaagtgtgaccatgacggggcccggtgatgcagagcttcaaggagtctcac	360	
Db	307	CGCTCCGAAGTGTGACCATGACCGGCGCCGGCTGATGCAGAGCTCAAGGAGTCTCAC	366	
Qy	361	tcccatgagtcctgctgagtcaccagcagtgctgctgagggcccttgagctcaacctggat	420	
Db	367	TCCCATGAGTCCCTGCTGAGTCCACAGCAGTGTGCTGAGGCCCTGGAGCTCAACCTGGAT	426	
Qy	421	gaagactccattatcaagccagtcacacagctcccatccttccttccttccttccttccttc	480	
Db	427	GAAGACTCCATTATCAAGCCAGTACACAGCTCCATCCTTGGCCAGGAGGTTCTGCTTTGAG	486	
Qy	481	gtaacaacatcgctctgggacaaaatgttttgcctgtcggttcgagccgaaaggacaaa	540	
Db	487	GTAACAACATCGTCTGGGACAAAAATGTTTTCCTGTCGGTCTGCAGCCGGAAGGACAAA	546	
Qy	541	tggattgagaatctacagagggtgtgaaaccccaacaaagacacagccgcgggtagat	600	
Db	547	TGGATTGAGAAATCTACAGAGGCTGTGAAACCCCAACAAAGGACAAACAGCCCGGGTAGAT	606	
Qy	601	aacgtgctgaaactatggatcatagaagctcgagagctgccccccaaagaagcgatat	660	
Db	607	AACGTGCTGAAACTATGGATCATAGAAAGCTCGAGAGCTGCCCCCCCCCAAGCGGATATTAC	666	

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BASE COUNT 936 a 1358 c 1203 g 768 t
ORIGIN

Query Match 94.8%; Score 3919; DB 74; Length 4265;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3942; Conservative 0; Mismatches 15; Indels 4; Gaps 1;

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Db 118 GCACCCCATTTCCCATTTGCTCCCCAGCAAGGCTTCCCTGAGCCGGAGGCTTAAAAAGCTCC 177
QY 238 atcaaacgtacaaagtacaaacccaaacttgaccggaccagcagctttccagacagatcccg 297
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DEFINITION Rattus norvegicus SynGAP-a mRNA, complete cds.
ACCESSION AF058789
VERSION AF058789.2 GI:10122137
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4539)
AUTHORS Kim, J. H., Liao, D., Lau, L. F. and Haganir, R. L.

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FEATURES

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Rattus norvegicus synaptic ras GTPase-activating protein p135

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AF048976.1

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Norway rat.

Rattus norvegicus

Chen,H.-J. and Kennedy,M.B.

Identification and cloning of a novel 130 kd protein containing a ras GTPase-activating domain from the rat forebrain postsynaptic density

(in) SOC. NEUROSCI. ABSTR.: 1466; (1997)

2 (bases 1 to 4063)

Chen,H.-J., Rojas-Soto,M. and Kennedy,M.B.

A synaptic Ras GTPase-activating protein (p135 SynGAP) inhibited by Cam kinase II

Unpublished

3 (bases 1 to 4063)

Chen,H.-J. and Kennedy,M.B.

Direct Submission

Submitted (17-FEB-1998) Division of Biology, California Institute of Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA 91125, USA

Location/Qualifiers

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Log to No. 4

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122. .4003

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/function="prominent substrate for endogenous CamKII; can activate intrinsic ras GTPase activity"

/note="synaptic ras-GAP; N-terminal encodes putative PH domain, C2 domain, and ras-GAP domain; C-terminal encodes proline-rich region, stretch of 10 histidine residues, and t/SXV motif; enriched in the forebrain postsynaptic density fraction"

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AUTHORS    Suzuki,T.
TITLE      SynGAP-d
JOURNAL    Published in DataBase (1999) In press
REFERENCE   2 (bases 1 to 4801)
AUTHORS    Suzuki,T.
TITLE      Direct Submission
JOURNAL    Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo
            Suzuki, Shinshu University School of Medicine, Department of
            Neuroplasticity; 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan
            (E-mail:suzuki@sch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683,
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RESULT 6

HSDJ570F3/c

LOCUS

DEFINITION

Human DNA sequence from clone RP4-570F3 on chromosome 6. Contains a gene similar to Rattus norvegicus synaptic ras GTPase-activating protein p135, the CICK0721Q.5 (polypeptide from patented cDNA Em:E06811) gene, the PHF1 (PHD finger protein 1) gene, the KNSL2 (kinesin-like 2) gene, the gene for acyl-protein thioesterase, ESTs, STSS, GSSs and a CpG island, complete sequence.

ACCESSION

AL050332

VERSION

AL050332.15 GI:6010176

KEYWORDS

HTG; CICK0721Q.5; CpG island; finger protein; GTPase-activating protein; kinesin-like; KNSL2; p135; PHD; PHF1; ribosomal protein L12; RPL12; Syngap.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 94770)

Direct Submission

TITLE

Submitted (17-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,

JOURNAL

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

COMMENT

requests: clonerequest@sanger.ac.uk
On Oct 4, 1999 this sequence version replaced gi:5870478.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP4-570F3 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP4-570F3. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone RP4-570F3 is at 1 in this sequence. The true left end of clone ICRF6c-CB2046 is at 94671 in this sequence. The true left end of clone ICRF6c-CK0721Q is at 20826 in this sequence. The true right end of clone ICRF6c-CK0721Q is at 61562 in this sequence.

FEATURES

source

Location/Qualifiers
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AL161903
AL161903.12 GI:10039702
HTG; HTGS_PHASE1; HTGS_DRAFT.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 150956)
Tracey, A.
Direct Submission
Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9796876.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bA175A4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 145680 bases at least Q40
Consensus quality: 147560 bases at least Q30
Consensus quality: 148600 bases at least Q20
Insert size: 150756; sum-of-contigs
Insert size: 148326; 10.8% error; agarose-fp
Quality coverage: 6.43x in Q20 bases; sum-of-contigs Quality
coverage: 6.54x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 54611: contig of 54611 bp in length
* 54612 54711: gap of 100 bp
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* 70294 70393: gap of 100 bp
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ORIGIN

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Best Local Similarity 91.0%; Pred. No. 1.1e-167;
Matches 979; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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VERSION AL161906.5 GI:9863619
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 169323)
JOURNAL Direct Submission
Submitted (17-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9212890.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA567N9
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 155424 bases at least Q40
Consensus quality: 160003 bases at least Q30
Insert size: 167023; sum-of-contigs
Insert size: 186175; 5.7% error; agarose-fp
Quality coverage: 3.59x in Q20 bases; sum-of-contigs Quality
coverage: 3.22x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 5456: contig of 5456 bp in length
* 5457 5556: gap of 100 bp
* 5557 8767: contig of 3211 bp in length
* 8768 8867: gap of 100 bp

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*	31189	31288: gap of 100 bp
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*	48355	48454: gap of 100 bp
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*	63402	63501: gap of 100 bp
*	63502	67724: contig of 4223 bp in length
*	67725	67824: gap of 100 bp
*	67825	70550: contig of 2726 bp in length
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*	70651	80664: contig of 10014 bp in length
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 829)
 AUTHORS Chen, H.-J. and Kennedy, M.B.
 TITLE Identification and cloning of a novel 130 kd protein containing a
 ras GTPase-activating domain from the rat forebrain postsynaptic
 density
 JOURNAL Abstr. Soc. Neurosci. 23, 1466-1466 (1997)
 REFERENCE 2 (bases 1 to 829)

AUTHORS Chen, H. J., Rojas-Soto, M., Oguni, A. and Kennedy, M. B.
 TITLE A synaptic Ras-GTPase activating protein (pl35 SynGAP) inhibited by
 Cam kinase II
 JOURNAL Neuron 20 (5), 895-904 (1998)
 MEDLINE 98282016
 REFERENCE 3 (bases 1 to 829)
 AUTHORS Chen, H.-J. and Kennedy, M. B.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-1998) Biology, California Institute of
 Technology, 1200 E. California Blvd., MC 216-76, Pasadena, CA
 91125, USA

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QY 61 ccacccgcccctctccgcccgcgctcctcctcctcctcctcctcctcctcctcctcctcctc 120
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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2884.142 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues
Total number of hits satisfying chosen parameters: 561672

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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2	63.4	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
3	62	1.5	3117	3	US-08-909-954-3	Sequence 3, Appli
4	61	1.5	2580	3	US-09-050-863-2	Sequence 2, Appli
5	61	1.5	5452	2	US-09-130-114-1	Sequence 1, Appli
6	61	1.5	10596	1	US-07-884-811-15	Sequence 15, Appl
7	61	1.5	10596	1	US-07-885-971-15	Sequence 15, Appl
8	61	1.5	10596	1	US-08-087-783A-15	Sequence 15, Appl
9	61	1.5	10596	1	US-08-194-088B-15	Sequence 15, Appl
10	61	1.5	10596	2	US-08-194-087-15	Sequence 15, Appl
11	61	1.5	10596	4	PCT-US93-04648-15	Sequence 15, Appl
12	57.6	1.4	2338	1	US-08-425-069-1	Sequence 1, Appli
13	57.6	1.4	2338	2	US-08-317-844B-1	Sequence 1, Appli
14	56	1.4	16442	3	US-08-781-891-208	Sequence 208, App
15	54.6	1.3	3489	2	US-08-728-323A-1	Sequence 1, Appli
16	54.6	1.3	32207	2	US-08-770-379-20	Sequence 20, Appl
17	54.4	1.3	9551	1	US-08-056-200-93	Sequence 93, Appl
18	54.4	1.3	9551	2	US-08-800-644-93	Sequence 93, Appl
19	54	1.3	543	5	5273901-6	Patent No. 5273901
20	53.6	1.3	1995	1	US-08-425-069-3	Sequence 3, Appli
21	53.6	1.3	1995	2	US-08-317-844B-3	Sequence 3, Appli
22	53	1.3	1137	5	5171843-8	Patent No. 5171843
23	52.2	1.3	1847	3	US-08-675-885-4	Sequence 4, Appli
24	51.4	1.2	697	5	5171843-10	Patent No. 5171843
25	51.4	1.2	152331	3	US-09-128-155-16	Sequence 16, Appl
26	51.2	1.2	2793	1	US-08-209-747-1	Sequence 1, Appli
27	51.2	1.2	2793	1	US-08-458-298-1	Sequence 1, Appli
28	51.2	1.2	51259	3	US-08-781-891-209	Sequence 209, App

29	49	1.2	2040	2	US-08-533-669A-5	Sequence 5, Appli
30	47.8	1.2	3337	1	US-08-072-610-1	Sequence 1, Appli
31	47.8	1.2	3337	2	US-08-719-822B-1	Sequence 1, Appli
32	47.6	1.2	397	3	US-09-253-691-3	Sequence 3, Appli
33	46	1.1	234	1	US-08-469-802B-3	Sequence 3, Appli
34	46	1.1	234	2	US-08-267-803B-3	Sequence 3, Appli
35	46	1.1	2818	1	US-08-366-276-1	Sequence 1, Appli
36	46	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
37	45	1.1	3456	1	US-08-190-687B-24	Sequence 24, Appl
38	45	1.1	4307	1	US-08-190-687B-7	Sequence 7, Appli
39	44.8	1.1	44377	2	US-08-804-227C-7	Sequence 7, Appli
40	44.8	1.1	44377	2	US-08-804-198-1	Sequence 1, Appli
41	44.6	1.1	533	5	5482709-5	Patent No. 5482709
42	44.4	1.1	1599	3	US-08-853-733B-1	Sequence 1, Appli
43	44.4	1.1	1603	3	US-08-675-885-6	Sequence 6, Appli
44	44.4	1.1	1931	2	US-09-130-114-2	Sequence 2, Appli
45	43.8	1.1	2385	1	US-08-393-333-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-909-954-1
; Sequence 1, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: GAP12 Genes and their Uses
; FILE REFERENCE: SEQ-11P
; CURRENT APPLICATION NUMBER: US/08/909,954A
; CURRENT FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3148
; TYPE: DNA
; ORGANISM: H. sapiens
US-08-909-954-1

Query Match 1.5%; Score 63.6; DB 3; Length 3148;
Best Local Similarity 50.0%; Pred. No. 7.4e-06;
Matches 159; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

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QY	1474	aaggtggtcaactcccattgctgtgttcccaggaggaggtgttgcacatgg	1533
Db	1578	tccgtggggcgtgcccgcgcacatgcctcgcctcaagcagctgcccgcgagtg	1637
QY	1534	cggctgcgtgtgcagagcgggggcgggaggacattgctgacaggctgacgcctcg	1593
Db	1638	gaggagcgttccccccagcggcagcaccaggtgtgaagtacctggccatcagtgatt	1697
QY	1594	ctcttcctgcgttctctctgcgcggcccatcgtgcgcagctgtgttgactgatgcag	1653
Db	1698	ctcttcttgcatcttctgcacctgcacatccttaccacaaagctgttgaccttcgggac	1757
QY	1654	gagtaccagatgagcagacctcagaaacccctcacccctacatcgccaaggttatccgaac	1713
Db	1758	caacacgcggacccccagactagcgcctcactgctgttcttgccaaggctgtgcagagc	1817
QY	1714	ctggccaaacttttccaag	1731
Db	1818	attggaacacctgggccag	1835

RESULT 2
US-08-232-463-14/c

/ COPY: 29,768
 / REGISTRATION NUMBER: 30472/114 IMM
 / REFERENCE/DOCKET NUMBER: 30472/114 IMM
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (703)836-9300
 / TELEFAX: (703)683-4109
 / TELEX: 899149
 / INFORMATION FOR SEQ ID NO: 14:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 7218 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / IMMEDIATE SOURCE:
 / CLONE: pTZgpt-Fls
 / US-08-232-463-14

Query Match	1.5%;	Score 62;	DB 3;	Length 3117;
Best Local Similarity	49.7%;	Pred. NO. 1.7e-05;		
Matches 158;	Conservative	0;	Mismatches 160;	Indels 0;
Gaps	0;			

QY	1414	gcgtccagtcgtgagagaccagggccaaacctgcggatgtgctgtgagttggccctgtgc	1473
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QY	1474	aaggtggtcaactcccatgtcggtgttcccgaggaggagctgaaggaggtgtttgcatcatcg	1533
Db	1407	tctacagggcgtgcccaottgccttgcgcttgccctttaagcagctccagcgggtgtgtg	1466
QY	1534	cggctgcgctgtgcagagcggggccggaggacattgctgacaggctgatcagcgcctcg	1593
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QY	1594	ctcttccctgcgcttccctgtgccggccatcatgtcgcccagtcgtgtttggactgatgcag	1653
Db	1527	ctcttctgcggttcttggcctgcccattcctcacaccgaaactgtttgacctcagagac	1586
QY	1654	gagtaccagatgagcagaaactcacgaacctcacacctcatcgccaaagttatccagaac	1713
Db	1587	cagcacgcagacccccagaccagccgttccctgtgctgctgcgcaaggctgtgcagagc	1646
QY	1714	ctggccaacttttccaa	1731
Db	1647	attgggaacctgggccag	1664

RESULT	4
US-09-050-863-2	
; Sequence 2, Application US/09050863	
; Patent No. 6114111	
; GENERAL INFORMATION:	
; APPLICANT: Lao, Ying	
; APPLICANT: Hiang, Betty	
; APPLICANT: Payan, Don	
; TITLE OF INVENTION: Mammalian Protein Interaction Cloning	
; TITLE OF INVENTION: System	
; NUMBER OF SEQUENCES: 5	
; CORRESPONDENCE ADDRESS:	
; ADDRESSEE: Flehr Hohbach, Test, Albritton & Herbert	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 07:58:32 ; Search time 6516.34 Seconds
(without alignments)
4445.587 Million cell updates/sec

Title: US-09-294-298-3
Perfect score: 4134
Sequence: 1 taaggccccccaccgacc.....tggggtgctatccccatcct 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 189: gb_est121:*

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 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	490.4	11.9	571	37	AV590698	AV590698 AV590698
2	383.8	9.3	474	181	AZ399131	AZ399131 IM0164P14
3	294.6	7.1	593	95	AW779747	AW779747 hn85f10.x
4	250.4	6.1	463	108	BE463433	BE463433 hw23d06.x
5	244.6	5.9	427	11	AA709010	AA709010 zf94h11.s
6	233.6	5.7	597	90	AW421227	AW421227 fj94f10.x
7	228.8	5.5	682	173	AQ993964	AQ993964 RPCI-23-2
8	222	5.4	566	22	AI606711	AI606711 ml58d01.y
9	221.8	5.4	413	10	AA691827	AA691827 vt05d01.r
10	214	5.2	707	28	AJ396547	AJ396547 AJ396547
11	211.8	5.1	555	27	AI958829	AI958829 fd22g01.y
12	201	4.9	628	108	BE490923	BE490923 db38g08.x
13	197.2	4.8	516	111	BE695645	BE695645 MR1-BT080
14	195.8	4.7	347	87	AW204612	AW204612 UI-H-B11-
15	195.4	4.7	596	136	BE848541	BE848541 uw39f05.y
16	190	4.6	481	135	BE773015	BE773015 RC1-FT013
17	185	4.5	542	93	AW656799	AW656799 109245 MA
18	182.2	4.4	296	23	AI650331	AI650331 wa18f01.x
19	177.6	4.3	345	39	AW076911	AW076911 fj03d08.y
20	173	4.2	511	22	AI577567	AI577567 UI-R-Y0-v
21	167.2	4.0	388	183	B68206	B68206 C1T978SK-A-
22	165.6	4.0	474	87	AW205989	AW205989 UI-H-B11-
23	161.2	3.9	460	22	AI609604	AI609604 tw91e09.x
24	157.8	3.8	1020	191	CNS02VGV	AL215753 Tetraodon
25	157	3.8	449	9	AA554056	AA554056 nl01g07.s
26	154.6	3.7	440	2	AA107246	AA107246 ml58d01.r
27	149.4	3.6	651	19	AI327335	AI327335 mp74c11.x
28	148.6	3.6	877	192	CNS04DL0	AL285885 Tetraodon
29	146.8	3.6	443	40	AW136165	AW136165 UI-H-B11-
30	146.8	3.6	464	95	AW826497	AW826497 fk62h05.x
31	146	3.5	452	9	AA554055	AA554055 nl01g06.s
32	145.4	3.5	407	133	BE015978	BE015978 fk62h05.y
33	139.8	3.4	382	22	AI562171	AI562171 vw73f04.x
34	138.6	3.4	317	91	AW527364	AW527364 UI-R-B01-
35	138.6	3.4	457	2	AA118397	AA118397 mp74c11.r
36	138.4	3.3	268	92	AW593427	AW593427 hg15e10.x
37	136.6	3.3	379	9	AA575948	AA575948 nm56e05.s
38	135.6	3.3	554	111	BE723198	BE723198 192621 MA
39	133.4	3.2	694	26	AI874961	AI874961 ul27f03.x
40	131.8	3.2	694	28	AJ399084	AJ399084 AJ399084
41	130.4	3.2	335	134	BE085114	BE085114 CM2-BT066
42	130	3.1	1006	190	CNS00HWF	AL073826 Drosophil
43	128.2	3.1	631	191	CNS01XQ5	AL172022 Tetraodon
44	126.8	3.1	975	191	CNS03ANH	AL235430 Tetraodon
45	124.2	3.0	397	111	BE695651	BE695651 MR1-BT080

ALIGNMENTS

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 LOCUS
 DEFINITION AV590698 Bos taurus brain fetus Bos taurus cDNA clone ElBR014B04
 5', mRNA sequence.
 ACCESSION AV590698
 VERSION AV590698.1 GI:9701691
 KEYWORDS EST.
 SOURCE cow.

QY 576 caaggacaacagccggttagataaacgtgctgaaactatggtatcatagaaagctcgaga 635
 Db 427 CCAGGACAACAGCCGCGAGTAGATAACGTGCTGAAGCTATGGATCATAGAGGCTCGAGA 368
 QY 636 gctgcccccaagaagagatattactgcagagttatgcctgcagacacatgctctatgcacg 695
 Db 367 GCTGCCCCCAAGAAGAGATATTACTGTGAGCTGTGCTGAGCAGACATGCTGTATGCACG 308
 QY 696 gaccacttccaaagcccgctcagcctcagcctcagcctcagcctcagcctcagcctcga 755
 Db 307 AACCACCTCCAAAGCCCGCTCGGCTTACGAGACACACCGTCTTTTGGGGGAGGACCTTTGA 248
 QY 756 gtttaacaacctgctgctgctccggcgctgcgctgcgctgcgctgcgctgcgctgcgcaaa 815
 Db 247 GTTTAAACAACCTGCTGCCGCTCCGGGCTTCCGGCTGCATGTGTACCGTGCATCAGACAA 188
 QY 816 aaagcggaagaaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcct 875
 Db 187 AAAGCGGAAGAAGGACAGGCTGGCTACGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 128
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 Db 127 AGCTGGGGCCCACTTCACAGAGCAGTGGTACCGCTGACCTTGCCTGACAGGACAGGCTGGGG 68
 QY 936 ctctggtgggtatggtgctgggggagagagagagagagagagagagagagagagagagag 995
 Db 67 CTCTGGGGGCTGGGCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8
 QY 996 gaaagga 1002
 Db 7 GAAAGGA 1

RESULT 3
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 DEFINITION similar to TR:095174 095174 NGAP. ;, mRNA sequence.
 ACCESSION AW779747
 VERSION AW779747.1 GI:7794350
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 593)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seg primer: -40Up from Gibco
 High quality sequence stop: 451.
 Location/Qualifiers
 1..593
 /organism="Homo sapiens"
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 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p77T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 104 a 169 c 178 g 141 t 1 others
 ORIGIN

Query Match 7.1%; Score 294.6; DB 95; Length 593;
 Best Local Similarity 73.0%; Pred. No. 6.3e-58;
 Matches 378; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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 QY 1054 cccatggagctatataagaggtttgcagaatatgtgaccaaccactaccgcatgctgtgt 1113
 Db 458 CCCATGGAGATGTACAAAGAGTTCGCTGAGCAGCATCACCAACCACTACCTGCTGGCTGTGT 399
 QY 1114 gccgtgctggagccgcccctcaatgtcaaggcgaaggaggtgcgtgtagtgcactggtt 1173
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 Db 158 TTCATCAAAAGCGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 99
 QY 1414 gcgtccagctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1473
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 QY 1474 aaggtggtcaactccattgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1511
 Db 38 AAGATCATCAACTCTTACTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1

RESULT 4
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 LOCUS BE463433 463 bp mRNA EST 27-JUL-2000
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 similar to TR:095174 095174 NGAP. ;, mRNA sequence.
 ACCESSION BE463433
 VERSION BE463433.1 GI:9509206
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 463)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -40UP from Gibco.

FEATURES
 source
 1. 463
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3183755"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 81 a 147 c 135 g 100 t
 ORIGIN

Query Match 6.1%; Score 250.4; DB 108; Length 463;
 Best Local Similarity 72.5%; Pred. No. 1.le-47;
 Matches 342; Conservative 0; Mismatches 121; Indels 9; Gaps 1;
 QY 342 gagcttcaaggagctcactccatgagtcctgctgagtcctcagcagctgctgagggc 401
 Db 463 GAGGCTGAAGGAGCTCGCTCCAGGAGTCCCTGCTCAGCCCCAGCAGTGGTGAGGC 404
 QY 402 cctggagctcaactggatgaagactccattatcaagccaggtacacagctccatcctggg 461
 Db 403 GCTGGACCTCAGCATGGAGGAGAGGTGGTGCATCAAGCCCGTGCACAGCAGCATCTGG 344
 QY 462 ccaggagttctgttggaggaacacatcgtctgtggacaaaatgtttgctgtcgtgc 521
 Db 343 CCAGGACTACTGCTTCGAGGTGACGACGTGCATCAGGAAGCAAGTGTCTTCTGCGCGTC 284
 QY 522 tgcagccgaaggacaaatgattgagaaatctacagagggctgtgaaacccaacaaagga 581
 Db 283 TGCAGCTGAGCGGGATAAGTGGATGGAGAACCTCCGCGGAGCGGTGCATCCCAACAGGA 224
 QY 582 caacagccggggtagataacgtgtgtaaaactatgatcatatagaagctcagagctgcc 641
 Db 223 CAACAGCCGGCGTGTGGAGCACATCTCTGAAGCTGTGGGTGATCGAGGCCAAGGACCTGCC 164
 QY 642 ccccaagaagcgtatattactgcgagttatgcctggagacatgctctatgcacggaccac 701
 Db 163 AGCCAAGAAGAAGTACCTGTGCGAGCTGTGCCTGGACGATGTCTCTATGCCCGCACCCAC 104
 QY 702 ttccaaagcccgctcagcctcagggagacactgtcttttggggcgagcacttcaggtttaa 761
 Db 103 GGGCAAGCTCAAGAC- -----GGACAAATGTTTTCGGGGCGGAGCAGTTCGAGTTCCA 53
 QY 762 caacctgcctgtgtccggcgctgcggctgcactatgtaccgtgactcggac 813
 Db 52 CAACTTGCCGCCCTCTGCGCACGGTCACTGTCCACCTGTACCCGGGAGACCGAC 1
 RESULT 5
 AA709010/c 427 bp mRNA EST 24-DEC-1997
 LOCUS
 DEFINITION zf94hl1.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:384645 3' similar to WP:007B5.1 CE00891 GTPASE-ACTIVATING PROTEIN ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AA709010
 AA709010.1 GI:2718928
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 I (bases 1 to 427)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 424.
 Location/Qualifiers
 1. 427

FEATURES
 source
 1. 427
 /organism="Homo sapiens"
 /db_xref="GDB:1292902"
 /db_xref="taxon:9606"
 /clone="IMAGE:384645"
 /clone_lib="Soares_pineal_gland_N3HPG"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: pineal gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCCGCTTTTCTTTTCTTTT 3']
 RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 77 a 118 c 127 g 104 t 1 others

Query Match 5.9%; Score 244.6; DB 11; Length 427;
 Best Local Similarity 75.0%; Pred. No. 2.4e-46;
 Matches 318; Conservative 0; Mismatches 105; Indels 1; Gaps 1;
 QY 1088 tgaccaaccactaccgcatgctgtgtgcgtgctgagccgcctcaatgtcaaggcca 1147
 Db 423 TCACCAACCCTACC-TGGGCTGTGTGAGCCCTCGAGCCCTCCTCAGTGCCCAAGACCA 365
 QY 1148 agggagggtcgctagtgcaactggttcacatcctgcaagcacaggccaaggact 1207
 Db 364 AGGAGGAGATTGCATCTGCCCTGGTGCACATCCTGCAGAGCAGCGGCAAGGTGAAGGACT 305
 QY 1208 tcccttcagacatggccatgtcagaggttagaccggttctatgagcgggaacacatcat 1267
 Db 304 TCCTGACAGACCTGATGATGTTCAGAGGTGAGCCGCTGCGGGGACAAACGAGCACCTCATCT 245
 QY 1268 tccgcgagaacacgctcgcctactaaagccatagaagagtatatgagactgattggccaga 1327
 Db 244 TCCGGGAGAACACANCTGCCACCAAGGCGATTGAGGAGTACCTCAAGCTAGTGGGCCAGA 185
 QY 1328 aatacctcaaggatgcccattggggagttcctccgggctctgtatgaatctgaggaact 1387
 Db 184 AGTACCTGCAGGACGCCCTAGGTGAGTTCATCAAGCGCTGTATGATGATGAGTGAAGAACT 125
 QY 1388 gtgaagtagaccccatcaagtgcacagctccagctcgtggcagagcaccagccaacctgc 1447
 Db 124 GCGAAGTGGATCCCAAGCAAGTGTCTCGGCGCTGACCTCCAGAGCACCAGGCAACCTCA 65


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Seq primer: T7
Class: BAC ends.

FEATURES             Location/Qualifiers
     1..682
         /organism="Mus musculus"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="RPCI-23-241C10"
         /clone_lib="RPCI-23"
         /sex="Female"
         /lab_host="DH10B"
         /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
         EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
         brain genomic DNA was isolated and partially digested
         with a combination of EcoRI and EcoRI Methylase. Size
         selected DNA was cloned into the pBACe3.6 vector at the
         EcoRI sites. The ligation products were transformed into
         DH10B electrocompetent cells (BRL Life Technologies)."
     169 a            190 c            146 g            176 t            "
                                     BASE COUNT

```

RESULT	8
AI606711	
LOCUS	AI606711 566 bp mRNA EST 15-MAR-2000
DEFINITION	ml58d01.y1 Stratagene mouse testis (#937308) Mus musculus cDNA
	clone IMAGE:516193 5' similar to TR:Q17774 Q17774 C07B5.1.; mRNA
	sequence.
ACCESSION	AI606711
VERSION	AI606711.1 GI:4615878
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 566)
AUTHORS	Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person , B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter , E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE	The WashU-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/WashU-NCI Mouse EST project 1999 Washington University School of Medicine 4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MGI:310041
Seq primer: -40RP from Gibco
High quality sequence stop: 414
POLYA=No.

FEATURES	Location/Qualifiers	source
	1. .566	
	/organism="Mus musculus"	
	/strain="Inbred CD-1"	
	/db_xref="taxon:10090"	
	/clone="IMAGE:516193"	
	/clone_lib="Stratagene mouse testis (#937308)"	
	/sex="males"	
	/tissue_type="testis"	
	/dev_stage="10-12 week old"	
	/lab_host="SOLR (kanamycin resistant)"	
	/note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Average insert size: 1.0 kb; Uni-ZAP XR vector; -5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."	
BASE COUNT	175 a 117 c 132 g 142 t	
ORIGIN		

RESULT	9
AA691827	
LOCUS	
DEFINITION	AA691827 413 bp mRNA EST 16-DEC-1997 vt05d01.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1162177 5' similar to WP:C07B5.1 CE00891 GTPASE-ACTIVATING PROTEIN ; mRNA sequence.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2001, 19:58:55 ; Search time 505.11 Seconds
(without alignments)
3074.557 Million cell updates/sec

Title: US-09-294-298-3
Perfect score: 4134
Sequence: 1 taagccccccccccgacc.....tgggggtgctatccccatcct 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36: *
1: /SIDS6/gcgdata/geneseq/geneseq/NA1980.DAT: *
2: /SIDS6/gcgdata/geneseq/geneseq/NA1981.DAT: *
3: /SIDS6/gcgdata/geneseq/geneseq/NA1982.DAT: *
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19: /SIDS6/gcgdata/geneseq/geneseq/NA1998.DAT: *
20: /SIDS6/gcgdata/geneseq/geneseq/NA1999.DAT: *
21: /SIDS6/gcgdata/geneseq/geneseq/NA2000.DAT: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query made 2.3% SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95.8	2.3	2647	18 T76739	CDNA encoding acti
2	63.6	1.5	1337	20 Z17263	Human gene express
3	61	1.5	795	19 V55830	FLGA insert stabl
4	61	1.5	799	19 V55831	Nucleotide sequenc
5	61	1.5	5452	20 X90923	Anti-sense strand
6	61	1.5	8705	20 Z23778	Vector pShuttle DN
7	61	1.5	9600	19 V21683	Vector plasmid pCM
8	61	1.5	10380	20 Z22248	Nucleotide sequenc
9	61	1.5	10596	14 Q51731	Plasmid pCisEBON f
10	61	1.5	10596	17 T40348	Plasmid pCisEBON f
11	61	1.5	10596	20 X15650	Nucleotide sequenc
12	59.6	1.4	1925	20 X90924	Epstein Barr Virus

13	59.4	1.4	1908	8 N71064	Gene encoding Plas
C 14	59.2	1.4	1000	21 A02484	Human colon cancer
C 15	57.8	1.4	49999	20 Z23895	Murine LOBO homolo
16	57.6	1.4	2338	19 V23249	Nephila clavipes s
17	57.6	1.4	2338	21 Z38195	N. clavipes spider
18	56	1.4	2000	8 N71065	Gene encoding Plas
19	56	1.4	2338	12 Q14183	N.clavipes draglin
C 20	56	1.4	16442	18 X83006	Partial mouse WRN
21	55.8	1.3	2004	18 T85356	Nephila clavipes s
C 22	54.6	1.3	32207	20 V73805	KSHV LUR DNA (nucl
C 23	54.6	1.3	137507	19 V19941	KSHV long unique c
24	54.4	1.3	9551	20 Z22301	CDNA encoding a hu
25	54	1.3	543	13 Q23092	Antigen tc-7a gene
26	53.6	1.3	1995	12 Q14184	N.clavipes draglin
27	53.6	1.3	1995	19 V23250	Nephila clavipes s
28	53.6	1.3	1995	21 Z38196	N. clavipes spider
29	53.4	1.3	4055	20 Z40484	Human ZC2 DNA. Ho
30	53.4	1.3	4180	21 A10669	Human protein kina
31	53	1.3	1137	14 Q33061	Plasmodium vivax c
C 32	52.6	1.3	10732	21 A10594	Gene encoding a su
C 33	52.4	1.3	114955	20 X53491	Human adenosine A1
34	52.2	1.3	1847	19 V04694	Cell cycle protein
35	51.4	1.2	3198	20 X02974	Human IL-1ra BAC c
36	51.2	1.2	2744	16 Q98470	MisP1-containing p
C 37	51.2	1.2	51259	18 X83007	Partial mouse WRN
38	50.2	1.2	1686	16 Q87587	DNA encoding Leuco
39	49	1.2	2040	18 T62137	Leishmania brazili
40	49	1.2	2040	19 V47557	Leishmania antigen
C 41	48.8	1.2	1218	21 A02488	Human colon cancer
42	48.8	1.2	2313	20 Z07197	Human lung tumour
43	48.6	1.2	1432	19 V47585	Leishmania antigen
44	47.8	1.2	3337	17 T34620	P. vivax ESP-1 blo
45	47.8	1.2	3337	20 X15174	DNA encoding a sec

ALIGNMENTS

RESULT 1	
T76739	
ID T76739 standard; CDNA; 2647 BP.	
XX	
AC T76739;	
XX	
DT 08-OCT-1997 (first entry)	
XX	
DE CDNA encoding active type R-Ras protein binding protein p98.	
XX	
KW Active-type-R-Ras protein; p98; tumour; disease; cancer;	
KW cellular Ca ion; phospholipid; tumour forming promoter;	
KW tumour forming inhibitor; ss.	
XX	
OS Bos taurus.	
XX	
FH Key	Location/Qualifiers
CDS	13..2517
FT	/*tag= a
FT	/product= p98
XX	
PN JP09135688-A.	
XX	
PD 27-MAY-1997.	
XX	
PF 16-NOV-1995; 95JP-0298720.	
XX	
PR 16-NOV-1995; 95JP-0298720.	
XX	
PA (KIRI) KIRIN BREWERY KK.	
XX	
DR WPI; 1997-335993/31.	
DR P-PSDB; W24227.	
XX	
PT Active R-Ras protein-binding protein p98 - used in the treatment of	

